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OM protein - protein search, using sw model

Run on: March 6, 2002, 13:35:19 ; Search time 14.19 Seconds
(without alignments)
1024.463 Million cell updates/sec

Title: US-09-405-504A-25
Perfect score: 3372
Sequence: 1 MRAPGAGAASVVSALLWLL.....HYLPLNEAVYTRICSGAFAL 646

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3372	100.0	646	4	US-09-232-200-25
2	3372	100.0	646	4	US-09-232-200-32
3	3372	100.0	646	4	US-09-232-200-38
4	3372	100.0	646	4	US-09-232-200-43
5	3372	100.0	646	4	US-09-232-200-47
6	3372	100.0	646	4	US-09-232-197-25
7	3372	100.0	646	4	US-09-232-197-32
8	3372	100.0	646	4	US-09-232-197-38
9	3372	100.0	646	4	US-09-232-197-43
10	3372	100.0	646	4	US-09-232-197-47
11	3062	90.8	646	4	US-09-232-200-59
12	3062	90.8	646	4	US-09-232-197-59
13	3057	90.7	646	4	US-09-232-200-92
14	3057	90.7	646	4	US-09-232-197-92
15	3054	90.6	646	4	US-09-232-200-33
16	3054	90.6	646	4	US-09-232-200-65
17	3054	90.6	646	4	US-09-232-197-33
18	3054	90.6	646	4	US-09-232-197-65
19	2119	62.8	643	4	US-09-232-200-27
20	2119	62.8	643	4	US-09-232-200-41
21	2119	62.8	643	4	US-09-232-200-53
22	2119	62.8	643	4	US-09-232-197-27
23	2119	62.8	643	4	US-09-232-197-41
24	2119	62.8	643	4	US-09-232-197-53
25	2114.5	62.7	632	4	US-09-232-200-34
26	2114.5	62.7	632	4	US-09-232-200-39
27	2114.5	62.7	632	4	US-09-232-197-34

ALIGNMENTS

RESULT 1

US-09-232-200-25
; Sequence 25, Application US/09232200A

; Patent No. 6288213

; GENERAL INFORMATION:

; APPLICANT: Stahl, Andreas

; APPLICANT: Hirsch, David J.

; APPLICANT: Lodish, Harvey F.

; APPLICANT: Gimeno, Ruth E.

; APPLICANT: Tartaglia, Louis A.

; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS

; FILE REFERENCE: WHI97-21p3MB

; CURRENT APPLICATION NUMBER: US/09/232,200A

; EARLIER FILING DATE: 1999-01-14

; EARLIER APPLICATION NUMBER: 60/071,374

; EARLIER FILING DATE: 1998-01-15

; EARLIER APPLICATION NUMBER: 60/093,491

; EARLIER FILING DATE: 1998-07-20

; EARLIER APPLICATION NUMBER: 60/110,941

; EARLIER FILING DATE: 1998-12-04

; NUMBER OF SEQ ID NOS: 105

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 25

; LENGTH: 646

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-232-200-25

Query Match 100.0%; Score 3372; DB 4; Length 646;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGAGAASVVSALLWLLGLPWTWSAAAALGVYVSGGWRFLRIYVCKTARRDLFGLSV 60

Db 1 MRAPGAGAASVVSALLWLLGLPWTWSAAAALGVYVSGGWRFLRIYVCKTARRDLFGLSV 60

QY 61 LIRVLELRHRHAGHTIPRIFQAVVORQPERLALVDAGTGCWTFQAQLDAYSNANLNF 120

Db 61 LIRVLELRHRHAGHTIPRIFQAVVORQPERLALVDAGTGCWTFQAQLDAYSNANLNF 120

QY 121 RQLGFAPGDVVAIFLEGRPEFVGLWGLAKAGMEALLNVNLRREPFLACLTSGAKALI 180

Db 121 RQLGFAPGDVVAIFLEGRPEFVGLWGLAKAGMEALLNVNLRREPFLACLTSGAKALI 180

QY 181 FGGEWAAVAEVSGLKSLIKFCSDGLGPEGLIPDTHLDPDLLKEASTAPLAQIPSKGM 240

Db 181 FGGEWAAVAEVSGLKSLIKFCSDGLGPEGLIPDTHLDPDLLKEASTAPLAQIPSKGM 240

QY 241 DDRLFYITSGTGLPKAAIVVHSHYRMAAFGHAYRMAQADVLDCLPLYHSAGNIIG 300

Sequence 39, Appl

Sequence 42, Appl

Sequence 42, Appl

Sequence 45, Appl

Sequence 45, Appl

Sequence 71, Appl

Sequence 35, Appl

Sequence 35, Appl

Sequence 9, Appl

Sequence 9, Appl

Sequence 95, Appl

Sequence 95, Appl

Sequence 63, Appl

Sequence 63, Appl

Sequence 1, Appl

Sequence 1, Appl

241	DDRLFYIYTSGITGLPKAAIVHSRYRWAAFGHHAYRMAQADVLYDCLPLVHSAGNIIG	300
301	VGQCLIVGLVIVLRKKFSASRWDDCIKYNTVVOYIGEICRYLLLKQPVREARRHRVRL	360
301	VGQCLIVGLVIVLRKKFSASRWDDCIKYNTVVOYIGEICRYLLLKQPVREARRHRVRL	360
361	AVGNGLRPAIWESEFTFERFGVROI GEFYGAT ECNCSIANMDGKVCSCGFNSRLPHVYP	420
361	AVGNGLRPAIWESEFTFERFGVROI GEFYGAT ECNCSIANMDGKVCSCGFNSRLPHVYP	420
421	LVKYNEDTMELLRDAOGLCIPQACEPGLLVGOINQODPLRRFDGYVSESATSKKTAHSV	480
421	LVKYNEDTMELLRDAOGLCIPQACEPGLLVGOINQODPLRRFDGYVSESATSKKTAHSV	480
481	FSKGDSAYLSGDLVLMDELGYMFRDRSGDTFRWRGENVSTTEVEGVLISLLGQTDVAY	540
481	FSKGDSAYLSGDLVLMDELGYMFRDRSGDTFRWRGENVSTTEVEGVLISLLGQTDVAY	540
541	GVAVPVGEGRAGMAAVDPHSLDPNAIYQELQKVLAPYARPIFLRLLPOVDVTGTFKIQ	600
541	GVAVPVGEGRAGMAAVDPHSLDPNAIYQELQKVLAPYARPIFLRLLPOVDVTGTFKIQ	600
601	KTRLREGFDPRTSDRLFFDLKOGHYLPLNEAVYTRICSGAFAL	646
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RESULT      2
US-09-232-200-32
; Sequence 32, Application US/09232200A
; Patent No. 6288213
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WH197-21d3MB
; CURRENT APPLICATION NUMBER: US/09/232,200A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-232-200-32

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181	QY	FGGEMVA	AEVSGH	LGSKSLIF	CGSDJG	PEGILPD	THLDPL	LKEAST	APLQIP	SKGM	240	
181	Db	FGGEMVA	AEVSGH	LGSKSLIF	CGSDJG	PEGILPD	THLDPL	LKEAST	APLQIP	SKGM	240	
241	QY	DDRFLY	ITSGTGL	PKAALV	HSRYRMA	AFGHAYR	MQAADV	LYDCL	PLYHSAG	NIIG	300	
241	Db	DDRFLY	ITSGTGL	PKAALV	HSRYRMA	AFGHAYR	MQAADV	LYDCL	PLYHSAG	NIIG	300	
301	QY	VGOCLY	TGLTWLR	KKFSASR	FWDDCI	KYCNCTV	VOYIGE	ICRYLL	KQPVRE	ARRHRVL	360	
301	Db	VGOCLY	TGLTWLR	KKFSASR	FWDDCI	KYCNCTV	VOYIGE	ICRYLL	KQPVRE	ARRHRVL	360	
361	QY	AVGNCL	RPAIWE	EFTFRFGY	VRQI	GEYPGAT	CNCISIAN	NKDGK	VGSCGF	NRSILPHVY	420	
361	Db	AVGNCL	RPAIWE	EFTFRFGY	VRQI	GEYPGAT	CNCISIAN	NKDGK	VGSCGF	NRSILPHVY	420	
421	QY	LVKYNED	TMELLR	DAQGLC	IPCQAG	PGLLVGO	I	INQDPL	RRFGYV	SESATSKKIA	480	
421	Db	LVKYNED	TMELLR	DAQGLC	IPCQAG	PGLLVGO	I	INQDPL	RRFGYV	SESATSKKIA	480	
481	QY	FSKGD	SAYLSG	DVLVMD	ELGYM	YFRDRSG	DTFRW	GENVST	TEVEGV	LSRLLG	QTDVAVY	540
481	Db	FSKGD	SAYLSG	DVLVMD	ELGYM	YFRDRSG	DTFRW	GENVST	TEVEGV	LSRLLG	QTDVAVY	540
541	QY	GVAPG	VGKAG	MAADP	SHSLDP	NAIYQ	ELQKVL	APYAR	I	FLRLLP	QVDDTGTG	600
541	Db	GVAPG	VGKAG	MAADP	SHSLDP	NAIYQ	ELQKVL	APYAR	I	FLRLLP	QVDDTGTG	600
601	QY	KTRLO	QEGFDP	PROT	SDRLFF	LDL	KOGHYL	PLNEAV	YTRICS	GAFAL	646	
601	Db	KTRLO	QEGFDP	PROT	SDRLFF	LDL	KOGHYL	PLNEAV	YTRICS	GAFAL	646	

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RESULT      3
US-09-232-200-38
; Sequence 38, Application US/092322200A
; Patent No. 6288213
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WHI97-21p3MB
; CURRENT APPLICATION NUMBER: US/09/232, 200A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-232-200-38

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGAGAAVSVSLALLMLGLPWTWSAAAALGVYVSGGWRFLRIYCKTARRDLFGLSV 60
DB 1 MRAPGAGAAVSVSLALLMLGLPWTWSAAAALGVYVSGGWRFLRIYCKTARRDLFGLSV 60
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DB 61 LIRVLELRHQRAGHTTIPRIQAVVQRPRLALVDAGTGEQWTFQAQLDAYSNVANLNF 120
QY 121 ROLGAPAGDVVAIFLEGPEFVGLWGLAKAGMEAAALLNVNLRREPFLAFCLGTSKAKALI 180
DB 121 ROLGAPAGDVVAIFLEGPEFVGLWGLAKAGMEAAALLNVNLRREPFLAFCLGTSKAKALI 180
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DB 181 FGGEMVAVAEVSCHLGSLLKFCSDGLGPEGILPDTHLLDPLLEKEASTAPLAQIPSKGM 240
QY 241 DDLRFYIYTSCTTGLPKAAIVVHSRYRMAAFGHAYRMAQADVLYDCLPLYHSAGNIIG 300
DB 241 DDLRFYIYTSCTTGLPKAAIVVHSRYRMAAFGHAYRMAQADVLYDCLPLYHSAGNIIG 300
QY 301 VGQCLLYGLTVLVRKKSASRFDWDCIKYNTVVOYIGEICRYLLKQPVREARRHRVRL 360
DB 301 VGQCLLYGLTVLVRKKSASRFDWDCIKYNTVVOYIGEICRYLLKQPVREARRHRVRL 360
QY 361 AVGNGLRPAIWEETFERFVGRIQGEFYGATECNCISANMDGKVGSCGFNSRILPHVYPIR 420
DB 361 AVGNGLRPAIWEETFERFVGRIQGEFYGATECNCISANMDGKVGSCGFNSRILPHVYPIR 420
QY 421 LVKVNEDTMELLRDAQGLCIPCOAGEPGLLVGINOQDPLRRFDGYSSESATSKIAHSV 480
DB 421 LVKVNEDTMELLRDAQGLCIPCOAGEPGLLVGINOQDPLRRFDGYSSESATSKIAHSV 480
QY 481 FSKGDSAYLSGVDVLMDELGYMYFRDRSGDTFRWGENVSTTEVEGVLRLGQTDVAVY 540
DB 481 FSKGDSAYLSGVDVLMDELGYMYFRDRSGDTFRWGENVSTTEVEGVLRLGQTDVAVY 540
QY 541 GVAVPGVEGKAGMAAVADPHSLDPNAYIQELQKVLAPYARPIFLRLLPQVDTTGTFTKI 600
DB 541 GVAVPGVEGKAGMAAVADPHSLDPNAYIQELQKVLAPYARPIFLRLLPQVDTTGTFTKI 600
QY 601 KTRLOREGFDPRTSDRLFFLDLKGHYLPLNEAVYTRICSGAFAL 646
DB 601 KTRLOREGFDPRTSDRLFFLDLKGHYLPLNEAVYTRICSGAFAL 646

RESULT 6
US-09-232-197-25
; Sequence 25, Application US/09232197A
; Patent No. 6300096
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WHI97-21p3MA
; CURRENT APPLICATION NUMBER: US/09/232,197A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER FILING DATE: 1998-07-20
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 646
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-232-197-25

Query Match 100.0%; Score 3372; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGAGAAVSVSLALLMLGLPWTWSAAAALGVYVSGGWRFLRIYCKTARRDLFGLSV 60
DB 1 MRAPGAGAAVSVSLALLMLGLPWTWSAAAALGVYVSGGWRFLRIYCKTARRDLFGLSV 60
QY 61 LIRVLELRHQRAGHTTIPRIQAVVQRPRLALVDAGTGEQWTFQAQLDAYSNVANLNF 120
DB 61 LIRVLELRHQRAGHTTIPRIQAVVQRPRLALVDAGTGEQWTFQAQLDAYSNVANLNF 120
QY 121 ROLGAPAGDVVAIFLEGPEFVGLWGLAKAGMEAAALLNVNLRREPFLAFCLGTSKAKALI 180
DB 121 ROLGAPAGDVVAIFLEGPEFVGLWGLAKAGMEAAALLNVNLRREPFLAFCLGTSKAKALI 180
QY 181 FGGEMVAVAEVSCHLGSLLKFCSDGLGPEGILPDTHLLDPLLEKEASTAPLAQIPSKGM 240
DB 181 FGGEMVAVAEVSCHLGSLLKFCSDGLGPEGILPDTHLLDPLLEKEASTAPLAQIPSKGM 240
QY 241 DDLRFYIYTSCTTGLPKAAIVVHSRYRMAAFGHAYRMAQADVLYDCLPLYHSAGNIIG 300
DB 241 DDLRFYIYTSCTTGLPKAAIVVHSRYRMAAFGHAYRMAQADVLYDCLPLYHSAGNIIG 300
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DB 301 VGQCLLYGLTVLVRKKSASRFDWDCIKYNTVVOYIGEICRYLLKQPVREARRHRVRL 360
QY 361 AVGNGLRPAIWEETFERFVGRIQGEFYGATECNCISANMDGKVGSCGFNSRILPHVYPIR 420
DB 361 AVGNGLRPAIWEETFERFVGRIQGEFYGATECNCISANMDGKVGSCGFNSRILPHVYPIR 420
QY 421 LVKVNEDTMELLRDAQGLCIPCOAGEPGLLVGINOQDPLRRFDGYSSESATSKIAHSV 480
DB 421 LVKVNEDTMELLRDAQGLCIPCOAGEPGLLVGINOQDPLRRFDGYSSESATSKIAHSV 480
QY 481 FSKGDSAYLSGVDVLMDELGYMYFRDRSGDTFRWGENVSTTEVEGVLRLGQTDVAVY 540
DB 481 FSKGDSAYLSGVDVLMDELGYMYFRDRSGDTFRWGENVSTTEVEGVLRLGQTDVAVY 540
QY 541 GVAVPGVEGKAGMAAVADPHSLDPNAYIQELQKVLAPYARPIFLRLLPQVDTTGTFTKI 600
DB 541 GVAVPGVEGKAGMAAVADPHSLDPNAYIQELQKVLAPYARPIFLRLLPQVDTTGTFTKI 600
QY 601 KTRLOREGFDPRTSDRLFFLDLKGHYLPLNEAVYTRICSGAFAL 646
DB 601 KTRLOREGFDPRTSDRLFFLDLKGHYLPLNEAVYTRICSGAFAL 646

RESULT 7
US-09-232-197-32
; Sequence 32, Application US/09232197A
; Patent No. 6300096
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WHI97-21p3MA
; CURRENT APPLICATION NUMBER: US/09/232,197A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
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NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-232-197-32

Query Match 100.0%; Score 3372; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MRAPGAGAAASVSLALLLGLPWTWSAAAALGVVYVGGWRFRLIVCKTARRDLFGLSV 60

QY 61 LIRVLELRHRRHAGHTIPRIFQAVVQROPRLALVDAGTGCCTFAQLDAYSNVANLF 120
DB 61 LIRVLELRHRRHAGHTIPRIFQAVVQROPRLALVDAGTGCCTFAQLDAYSNVANLF 120

QY 121 RQLGFAPGDVVAIFLEGRPEFVGLWGLAKAGMEALLNVNLRREPFLAFCGLTSGAKALI 180
DB 121 RQLGFAPGDVVAIFLEGRPEFVGLWGLAKAGMEALLNVNLRREPFLAFCGLTSGAKALI 180

QY 181 FGGEMVAAYAEVSGHLGKSLIKFCSDGLPGLPDLTHLLDPLLEKASTAPLAQIPSKGM 240
DB 181 FGGEMVAAYAEVSGHLGKSLIKFCSDGLPGLPDLTHLLDPLLEKASTAPLAQIPSKGM 240

QY 241 DDLRFYIYTSGLTPKAAIVVHSRYRMAAFGHAYRMAQAAADVLYDCLPLYHSAGNIIG 300
DB 241 DDLRFYIYTSGLTPKAAIVVHSRYRMAAFGHAYRMAQAAADVLYDCLPLYHSAGNIIG 300

QY 301 VGQCLLYGLTVLVRKFSASRFWDCCIYKNTVVOYIGEICRYLLKQPVREARRHRVRL 360
DB 301 VGQCLLYGLTVLVRKFSASRFWDCCIYKNTVVOYIGEICRYLLKQPVREARRHRVRL 360

QY 361 AVGNGLRPAIWEETFERFVGRIQGEFYGATECNCSIANMDKVGSCGNSRLIPHYPIR 420
DB 361 AVGNGLRPAIWEETFERFVGRIQGEFYGATECNCSIANMDKVGSCGNSRLIPHYPIR 420

QY 421 LKVNEDTMELLRDAQGLCIPCOAGEPGLLVGOINQODPLRRFDGYVSESATSKIAHSV 480
DB 421 LKVNEDTMELLRDAQGLCIPCOAGEPGLLVGOINQODPLRRFDGYVSESATSKIAHSV 480

QY 481 FSKGDSAYLSGDVLYMDELGYMYFRDRSGDTFRWGENVSTTEVEGVLRLGQTDVAVY 540
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QY 541 GVAVPGVEGKAGMAAVADPHSLDDPNAIYQELQKVLAPYARPIFLRLLPQVDTTGTFTKIQ 600
DB 541 GVAVPGVEGKAGMAAVADPHSLDDPNAIYQELQKVLAPYARPIFLRLLPQVDTTGTFTKIQ 600

QY 601 KTRLOREGFDPRTSDRLFFLDLKQGHYLPNEAVYTRICSGAFAL 646
DB 601 KTRLOREGFDPRTSDRLFFLDLKQGHYLPNEAVYTRICSGAFAL 646

RESULT 8

US-09-232-197-38
; Sequence 38, Application US/09232197A
; Patent No. 6300096
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WHI97-21p3MA
; CURRENT APPLICATION NUMBER: US/09/232.197A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374

EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-232-197-38

Query Match 100.0%; Score 3372; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGAGAAASVSLALLLGLPWTWSAAAALGVVYVGGWRFRLIVCKTARRDLFGLSV 60
DB 1 MRAPGAGAAASVSLALLLGLPWTWSAAAALGVVYVGGWRFRLIVCKTARRDLFGLSV 60

QY 61 LIRVLELRHRRHAGHTIPRIFQAVVQROPRLALVDAGTGCCTFAQLDAYSNVANLF 120
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DB 121 RQLGFAPGDVVAIFLEGRPEFVGLWGLAKAGMEALLNVNLRREPFLAFCGLTSGAKALI 180

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QY 241 DDLRFYIYTSGLTPKAAIVVHSRYRMAAFGHAYRMAQAAADVLYDCLPLYHSAGNIIG 300
DB 241 DDLRFYIYTSGLTPKAAIVVHSRYRMAAFGHAYRMAQAAADVLYDCLPLYHSAGNIIG 300

QY 301 VGQCLLYGLTVLVRKFSASRFWDCCIYKNTVVOYIGEICRYLLKQPVREARRHRVRL 360
DB 301 VGQCLLYGLTVLVRKFSASRFWDCCIYKNTVVOYIGEICRYLLKQPVREARRHRVRL 360

QY 361 AVGNGLRPAIWEETFERFVGRIQGEFYGATECNCSIANMDKVGSCGNSRLIPHYPIR 420
DB 361 AVGNGLRPAIWEETFERFVGRIQGEFYGATECNCSIANMDKVGSCGNSRLIPHYPIR 420

QY 421 LKVNEDTMELLRDAQGLCIPCOAGEPGLLVGOINQODPLRRFDGYVSESATSKIAHSV 480
DB 421 LKVNEDTMELLRDAQGLCIPCOAGEPGLLVGOINQODPLRRFDGYVSESATSKIAHSV 480

QY 481 FSKGDSAYLSGDVLYMDELGYMYFRDRSGDTFRWGENVSTTEVEGVLRLGQTDVAVY 540
DB 481 FSKGDSAYLSGDVLYMDELGYMYFRDRSGDTFRWGENVSTTEVEGVLRLGQTDVAVY 540

QY 541 GVAVPGVEGKAGMAAVADPHSLDDPNAIYQELQKVLAPYARPIFLRLLPQVDTTGTFTKIQ 600
DB 541 GVAVPGVEGKAGMAAVADPHSLDDPNAIYQELQKVLAPYARPIFLRLLPQVDTTGTFTKIQ 600

QY 601 KTRLOREGFDPRTSDRLFFLDLKQGHYLPNEAVYTRICSGAFAL 646
DB 601 KTRLOREGFDPRTSDRLFFLDLKQGHYLPNEAVYTRICSGAFAL 646

RESULT 9

US-09-232-197-43
; Sequence 43, Application US/09232197A
; Patent No. 6300096
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.

; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WH197-21p3MA
; CURRENT APPLICATION NUMBER: US/09/232,197A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-232-197-43

Query Match 100.0%; Score 3372; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGAGAAVSVSLALLLGLPWTWSAAALGVVYVGGWRFRLIVCKTARRDLFGLSV 60
Db 1 MRAPGAGAAVSVSLALLLGLPWTWSAAALGVVYVGGWRFRLIVCKTARRDLFGLSV 60

QY 61 LIRVLELRHQRAGHTIPRIFQAVVQRPRLALVDAGTGEQWTFQAOLDAYSNAVANLF 120
Db 61 LIRVLELRHQRAGHTIPRIFQAVVQRPRLALVDAGTGEQWTFQAOLDAYSNAVANLF 120

QY 121 RQLGFAPGDVVAIFLEGPRFEVGLWGLAKAGMEALLNVNLRREPLAFCLGTSGAKALI 180
Db 121 RQLGFAPGDVVAIFLEGPRFEVGLWGLAKAGMEALLNVNLRREPLAFCLGTSGAKALI 180

QY 181 FGGEMVAAVAEVSCHLGLKSLKFCSDGLGPEGLPDTLLDPLKEASTAPLAQIPSKGM 240
Db 181 FGGEMVAAVAEVSCHLGLKSLKFCSDGLGPEGLPDTLLDPLKEASTAPLAQIPSKGM 240

QY 241 DDRLFYITSGTTGLPKAAIVVHSRYRMAAFGHAYRMAAADVLYDCLPLYHSAGNIIG 300
Db 241 DDRLFYITSGTTGLPKAAIVVHSRYRMAAFGHAYRMAAADVLYDCLPLYHSAGNIIG 300

QY 301 VGOCILYGLTVLVRKKFSASRFWDDCIKYNCTVQYIGEICRYLLKQPVREARRHRVRL 360
Db 301 VGOCILYGLTVLVRKKFSASRFWDDCIKYNCTVQYIGEICRYLLKQPVREARRHRVRL 360

QY 361 AVGNGLRPAIWEETFERFVQRIQGEFYGATECNCSTANMDGKVGSCGFNSRLPHVYPPIR 420
Db 421 AVGNGLRPAIWEETFERFVQRIQGEFYGATECNCSTANMDGKVGSCGFNSRLPHVYPPIR 420

QY 421 LVKVNEDTMELLRDAQGLCIPCOAGEPGLLVQIINQDPLRRFDGYSVSEATSKKIAHSV 480
Db 421 LVKVNEDTMELLRDAQGLCIPCOAGEPGLLVQIINQDPLRRFDGYSVSEATSKKIAHSV 480

QY 481 FSKGDSAYLSGDVLYVMDDELGYMYFRDRSGDTFRWGENVSTTEVEGVLRLGQTDVAVY 540
Db 481 FSKGDSAYLSGDVLYVMDDELGYMYFRDRSGDTFRWGENVSTTEVEGVLRLGQTDVAVY 540

QY 541 GVAVPGEVKAGMAAADPHSLDNPNAIYQELQKVLAPYARPIFLRLLPQVDTTGTFKIQ 600
Db 541 GVAVPGEVKAGMAAADPHSLDNPNAIYQELQKVLAPYARPIFLRLLPQVDTTGTFKIQ 600

QY 601 KTRLOREGFDPQTSRDLFFLDLKQGHYLPNEAVYTRICSGAFAL 646
Db 601 KTRLOREGFDPQTSRDLFFLDLKQGHYLPNEAVYTRICSGAFAL 646

RESULT 10

US-09-232-197-47
; Sequence 47, Application US/09232197A
; Patent No. 630096
; GENERAL INFORMATION:

; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WH197-21p3MA
; CURRENT APPLICATION NUMBER: US/09/232,197A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-232-197-47

Query Match 100.0%; Score 3372; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGAGAAVSVSLALLLGLPWTWSAAALGVVYVGGWRFRLIVCKTARRDLFGLSV 60
Db 1 MRAPGAGAAVSVSLALLLGLPWTWSAAALGVVYVGGWRFRLIVCKTARRDLFGLSV 60

QY 61 LIRVLELRHQRAGHTIPRIFQAVVQRPRLALVDAGTGEQWTFQAOLDAYSNAVANLF 120
Db 61 LIRVLELRHQRAGHTIPRIFQAVVQRPRLALVDAGTGEQWTFQAOLDAYSNAVANLF 120

QY 121 RQLGFAPGDVVAIFLEGPRFEVGLWGLAKAGMEALLNVNLRREPLAFCLGTSGAKALI 180
Db 121 RQLGFAPGDVVAIFLEGPRFEVGLWGLAKAGMEALLNVNLRREPLAFCLGTSGAKALI 180

QY 181 FGGEMVAAVAEVSCHLGLKSLKFCSDGLGPEGLPDTLLDPLKEASTAPLAQIPSKGM 240
Db 181 FGGEMVAAVAEVSCHLGLKSLKFCSDGLGPEGLPDTLLDPLKEASTAPLAQIPSKGM 240

QY 241 DDRLFYITSGTTGLPKAAIVVHSRYRMAAFGHAYRMAAADVLYDCLPLYHSAGNIIG 300
Db 241 DDRLFYITSGTTGLPKAAIVVHSRYRMAAFGHAYRMAAADVLYDCLPLYHSAGNIIG 300

QY 301 VGOCILYGLTVLVRKKFSASRFWDDCIKYNCTVQYIGEICRYLLKQPVREARRHRVRL 360
Db 301 VGOCILYGLTVLVRKKFSASRFWDDCIKYNCTVQYIGEICRYLLKQPVREARRHRVRL 360

QY 361 AVGNGLRPAIWEETFERFVQRIQGEFYGATECNCSTANMDGKVGSCGFNSRLPHVYPPIR 420
Db 361 AVGNGLRPAIWEETFERFVQRIQGEFYGATECNCSTANMDGKVGSCGFNSRLPHVYPPIR 420

QY 421 LVKVNEDTMELLRDAQGLCIPCOAGEPGLLVQIINQDPLRRFDGYSVSEATSKKIAHSV 480
Db 421 LVKVNEDTMELLRDAQGLCIPCOAGEPGLLVQIINQDPLRRFDGYSVSEATSKKIAHSV 480

QY 481 FSKGDSAYLSGDVLYVMDDELGYMYFRDRSGDTFRWGENVSTTEVEGVLRLGQTDVAVY 540
Db 481 FSKGDSAYLSGDVLYVMDDELGYMYFRDRSGDTFRWGENVSTTEVEGVLRLGQTDVAVY 540

QY 541 GVAVPGEVKAGMAAADPHSLDNPNAIYQELQKVLAPYARPIFLRLLPQVDTTGTFKIQ 600
Db 541 GVAVPGEVKAGMAAADPHSLDNPNAIYQELQKVLAPYARPIFLRLLPQVDTTGTFKIQ 600

QY 601 KTRLOREGFDPQTSRDLFFLDLKQGHYLPNEAVYTRICSGAFAL 646
Db 601 KTRLOREGFDPQTSRDLFFLDLKQGHYLPNEAVYTRICSGAFAL 646

RESULT 11

US-09-232-200-59
 ; Sequence 59, Application US/09232200A
 ; Patent No. 6288213
 ; GENERAL INFORMATION:
 ; APPLICANT: Stahl, Andreas
 ; APPLICANT: Hirsch, David J.
 ; APPLICANT: Lodish, Harvey F.
 ; APPLICANT: Gimeno, Ruth E.
 ; APPLICANT: Tartaglia, Louis A.
 ; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
 ; FILE REFERENCE: WH197-21p3MB
 ; CURRENT APPLICATION NUMBER: US/09/232,200A
 ; EARLIER FILING DATE: 1999-01-14
 ; EARLIER APPLICATION NUMBER: 60/071,374
 ; EARLIER FILING DATE: 1998-01-15
 ; EARLIER APPLICATION NUMBER: 60/093,491
 ; EARLIER FILING DATE: 1998-07-20
 ; EARLIER APPLICATION NUMBER: 60/110,941
 ; EARLIER FILING DATE: 1998-12-04
 ; NUMBER OF SEQ ID NOS: 105
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 59
 ; LENGTH: 646
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-09-232-200-59

Query Match 90.8%; Score 3062; DB 4; Length 646;
 Best Local Similarity 89.5%; Pred. No. 0;

Matches 578; Conservative 30; Mismatches 38; Indels 0; Gaps 0;

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QY 1 MRAPGAGAAVSYSLLALLWLLGLPWTWSAAAALGVVVGSGWRFLRIVCKTARRDLFGLSV 60
DQ 1 MRPAGAGTASVSLGLLWLLGLPWTWSAAAALGVVVGSGWRFLRIVCKTARRDLFGLSV 60

QY 61 LIRVLELRHRRAGHTIPRIFOAVVQRPRLALVDAGTGCWTFQAOLDYSNAVANLF 120
DQ 61 LIRVLELRHRRAGHTIPRIFOAVVQRPRLALVDAGTGCWTFQAOLDYSNAVANLF 120

QY 121 ROLGAPGDVVAIFLEGRPEFVGLWGLAKAGMEALLNVNLRREPLAFCLGTSGAKALI 180
DQ 121 ROLGAPGDVVAIFLEGRPEFVGLWGLAKAGMEALLNVNLRREPLAFCLGTSGAKALI 180

QY 181 FCGEMVAVAEVSCHLGSLLKFCSDGLGPEGLPDTLLDPLKKEASTAPLAQIPSKGM 240
DQ 181 YGEMAAVAEVSCHLGSLLKFCSDGLGPEGLPDTLLDPLKKEASTAPLAQIPSKGM 240

QY 241 DRLFYIYTSGLTGLPKAAIVVHSRYRMAAFGHGHHAYRMAADVLYDCLPLHYSAGNIIG 300
DQ 241 DRLFYIYTSGLTGLPKAAIVVHSRYRMAAFGHGHHAYRMAADVLYDCLPLHYSAGNIIG 300

QY 301 VGQCIIYGLTVLVRKFSASRFDWDCIKYNTVVOYIGEICRYLLKQPVREARRHRVRL 360
DQ 301 VGQCIIYGLTVLVRKFSASRFDWDCIKYNTVVOYIGEICRYLLKQPVREARRHRVRL 360

QY 361 AVGNGLRPAIWEETFEFGRVQIGEFYGATECNCNANMDKGVSCGFNSRILPHVYPIR 420
DQ 361 AVGNGLRPAIWEETFEFGRVQIGEFYGATECNCNANMDKGVSCGFNSRILPHVYPIR 420

QY 421 LKVNEDTMELLRDAQGLCIPQAGEPGLLVGOINQODPLRRFDGVVSESATSKIAHSV 480
DQ 421 LKVNEDTMELLRDAQGLCIPQAGEPGLLVGOINQODPLRRFDGVVSESATSKIAHSV 480

QY 481 FSKGDSAYLSGDVLMDELGYMYFRDRSGDTFRWGENYSTTEVEGVLRLGQTDVAVY 540
DQ 481 FSKGDSAYLSGDVLMDELGYMYFRDRSGDTFRWGENYSTTEVEGVLRLGQTDVAVY 540

QY 541 GVAVPGVEGKAGMAVADPHSLDPNATYQELQKVLAPYARPIFLRLLPQVDTTGTFKIQ 600
DQ 541 GVAVPGVEGKAGMAVADPHSLDPNATYQELQKVLAPYARPIFLRLLPQVDTTGTFKIQ 600

```

QY 601 KTRIQREGFDPRQTSRDLFFLDLKGHYLPLNEAVYTRICSGAFAL 646
 DQ 601 KTRIQREGFDPRQTSRDLFFLDLKGHYLPLNEAVYTRICSGAFAL 646

RESULT 12

US-09-232-197-59
 ; Sequence 59, Application US/09232197A
 ; Patent No. 6300096
 ; GENERAL INFORMATION:
 ; APPLICANT: Stahl, Andreas
 ; APPLICANT: Hirsch, David J.
 ; APPLICANT: Lodish, Harvey F.
 ; APPLICANT: Gimeno, Ruth E.
 ; APPLICANT: Tartaglia, Louis A.
 ; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
 ; FILE REFERENCE: WH197-21p3MA
 ; CURRENT APPLICATION NUMBER: US/09/232,197A
 ; EARLIER FILING DATE: 1999-01-14
 ; EARLIER APPLICATION NUMBER: 60/071,374
 ; EARLIER FILING DATE: 1998-01-15
 ; EARLIER APPLICATION NUMBER: 60/093,491
 ; EARLIER FILING DATE: 1998-07-20
 ; EARLIER APPLICATION NUMBER: 60/110,941
 ; EARLIER FILING DATE: 1998-12-04
 ; NUMBER OF SEQ ID NOS: 105
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 59
 ; LENGTH: 646
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-09-232-197-59

Query Match 90.8%; Score 3062; DB 4; Length 646;
 Best Local Similarity 89.5%; Pred. No. 0;

Matches 578; Conservative 30; Mismatches 38; Indels 0; Gaps 0;

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QY 1 MRAPGAGAAVSYSLLALLWLLGLPWTWSAAAALGVVVGSGWRFLRIVCKTARRDLFGLSV 60
DQ 1 MRPAGAGTASVSLGLLWLLGLPWTWSAAAALGVVVGSGWRFLRIVCKTARRDLFGLSV 60

QY 61 LIRVLELRHRRAGHTIPRIFOAVVQRPRLALVDAGTGCWTFQAOLDYSNAVANLF 120
DQ 61 LIRVLELRHRRAGHTIPRIFOAVVQRPRLALVDAGTGCWTFQAOLDYSNAVANLF 120

QY 121 ROLGAPGDVVAIFLEGRPEFVGLWGLAKAGMEALLNVNLRREPLAFCLGTSGAKALI 180
DQ 121 ROLGAPGDVVAIFLEGRPEFVGLWGLAKAGMEALLNVNLRREPLAFCLGTSGAKALI 180

QY 181 FCGEMVAVAEVSCHLGSLLKFCSDGLGPEGLPDTLLDPLKKEASTAPLAQIPSKGM 240
DQ 181 YGEMAAVAEVSCHLGSLLKFCSDGLGPEGLPDTLLDPLKKEASTAPLAQIPSKGM 240

QY 241 DRLFYIYTSGLTGLPKAAIVVHSRYRMAAFGHGHHAYRMAADVLYDCLPLHYSAGNIIG 300
DQ 241 DRLFYIYTSGLTGLPKAAIVVHSRYRMAAFGHGHHAYRMAADVLYDCLPLHYSAGNIIG 300

QY 301 VGQCIIYGLTVLVRKFSASRFDWDCIKYNTVVOYIGEICRYLLKQPVREARRHRVRL 360
DQ 301 VGQCIIYGLTVLVRKFSASRFDWDCIKYNTVVOYIGEICRYLLKQPVREARRHRVRL 360

QY 361 AVGNGLRPAIWEETFEFGRVQIGEFYGATECNCNANMDKGVSCGFNSRILPHVYPIR 420
DQ 361 AVGNGLRPAIWEETFEFGRVQIGEFYGATECNCNANMDKGVSCGFNSRILPHVYPIR 420

QY 421 LKVNEDTMELLRDAQGLCIPQAGEPGLLVGOINQODPLRRFDGVVSESATSKIAHSV 480
DQ 421 LKVNEDTMELLRDAQGLCIPQAGEPGLLVGOINQODPLRRFDGVVSESATSKIAHSV 480

QY 481 FSKGDSAYLSGDVLMDELGYMYFRDRSGDTFRWGENYSTTEVEGVLRLGQTDVAVY 540
DQ 481 FSKGDSAYLSGDVLMDELGYMYFRDRSGDTFRWGENYSTTEVEGVLRLGQTDVAVY 540

```


Db 361 AVGNGLRPAIWEETQRFVGPQIGEFYGATECNCSTANMDGKVGSCGFNSRIILTHVYPIR 420
QY 421 LVKVNEDTMELLRDAGCLTIPCQAGPGLLVGQINQODPLRRFDGYVSESATSKKTAHSV 480
Db 421 LVKVNEDTMELPLRDSGLTIPCQGPGLLVGQINQODPLRRFDGYVSDSATNKKTAHSV 480
QY 481 FSKGDSAYLSGDLVMDLGYMYFRDRSGDTFRWRGENYSTTEVEGVLRRLLGQTDVAVY 540
Db 481 FRKGD SAYLSGDLVMDLGYMYFRDRSGDTFRWRGENYSTTEVEAVLSRLLGQTDVAVY 540
QY 541 GVAVPGVEGKAGMAAVADPHSLDDPNATYQELQKVLAPYARPIFLRLLPQVDTTGTFKIQ 600
Db 541 GVAVPGVEGKAGMAAIADPHSQLDPNSMYQELQKVLASVYARPIFLRLLPQVDTTGTFKIQ 600
QY 601 KTRLOREGFDPRTSDRLFLDLKQGHYLPNEAVYTRICSGAFAL 646
Db 601 KTRLOREGFDPRTSDRLFLDLKQGRYLPDLDERVHARICAGDFSL 646

RESULT 15

US-09-232-200-33
; Sequence 33, Application US/09232200A
; Patent No. 6288213
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WHI97-21p3MB
; CURRENT APPLICATION NUMBER: US/09/232,200A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-232-200-33

Query Match 90.6%; Score 3054; DB 4; Length 646;
Best Local Similarity 89.5%; Pred. No. 0;
Matches 578; Conservative 30; Mismatches 38; Indels 0; Gaps 0;
QY 1 MRAPGAGAAVSVLALLMLGLPTWTSAAAALGVYVGGWRFRIIVCKTARRDLFGLSV 60
Db 1 MRAPGAGTASVALLMLGLPTWTSAAAALGVYVGGWRFRIIVCKTARRDLFGLSV 60
QY 61 LIRVLELRRHORAGHTIPRIFQAVVQRPRLALVDAGTCECWTFAQLDAYSNVANLF 120
Db 61 LIRVLELRRHORAGHTIPRIFQAVVQRPRLALVDAGTCECWTFAQLDAYSNVANLF 120
QY 121 ROLGAPGVVAVIFLEGPEFVGLWGLAKAGMEAAALLNVNLRREPLAFCLGTSKAKALI 180
Db 121 ROLGAPGVVAVIFLEGPEFVGLWGLAKAGVVAALLNVNLRREPLAFCLGTSKAKALI 180
QY 181 FGGEMVAVAEVSGLKSLIKFCSGDLGPEGILPDTHLLDPLLKEASTAPLAQIPSKGM 240
Db 181 YGGENAAAAEVSQGLSKSLIKFCSGDLGPEGILPDTHLLDPLLKEASTAPLAQIPSKGM 240
QY 241 DDLRFYIYTSGLTPKAAIIVVHSRYVMAAFGHYHAYRMAQAAVDLYDCLPLYSAGNIIG 300
Db 241 DDLRFYIYTSGLTPKAAIIVVHSRYVMAAFGHYHAYRMAQAAVDLYDCLPLYSAGNIIG 300

QY 301 VQOCLLYGLTVLRRKFSASRFWDCKIKYNTVVQYIIGEICRYLLKQPVREARRHRVRL 360
Db 301 VQOCLLYGLTVLRRKFSASRFWDCKIKYNTVVQYIIGEICRYLLKQPVREARRHRVRL 360
QY 361 AVGNGLRPAIWEETQRFVGPQIGEFYGATECNCSTANMDGKVGSCGFNSRIILPHVYPIR 420
Db 361 AVGNGLRPAIWEETQRFVGPQIGEFYGATECNCSTANMDGKVGSCGFNSRIILPHVYPIR 420
QY 421 LVKVNEDTMELLRDAGCLTIPCQAGPGLLVGQINQODPLRRFDGYVSESATSKKTAHSV 480
Db 421 LVKVNEDTMELPLRDSGLTIPCQGPGLLVGQINQODPLRRFDGYVSDSATNKKTAHSV 480
QY 481 FSKGDSAYLSGDLVMDLGYMYFRDRSGDTFRWRGENYSTTEVEGVLRRLLGQTDVAVY 540
Db 481 FRKGD SAYLSGDLVMDLGYMYFRDRSGDTFRWRGENYSTTEVEAVLSRLLGQTDVAVY 540
QY 541 GVAVPGVEGKAGMAAVADPHSLDDPNATYQELQKVLAPYARPIFLRLLPQVDTTGTFKIQ 600
Db 541 GVAVPGVEGKAGMAAIADPHSQLDPNSMYQELQKVLASVYARPIFLRLLPQVDTTGTFKIQ 600
QY 601 KTRLOREGFDPRTSDRLFLDLKQGHYLPNEAVYTRICSGAFAL 646
Db 601 KTRLOREGFDPRTSDRLFLDLKQGRYLPDLDERVHARICAGDFSL 646

Search completed: March 6, 2002, 13:38:48
Job time: 209 sec

Db 490 GKPCLLTKIRKNQPFGLYRG--SODETKRKLVANVRQVGDLYNTYNTGVDLALDQGRFFYF 547

QY 505 RDRSGDTRWRGNSVTEVEGVSRLGLQTDVAVYGVAVGVGKAGMAAV-ADPHSL 563

Db 548 RDLGDTFRWKNSTREVEGVSILDFLEEVNIGVYVPGCEGKVGMAAVKLAPGKTF 607

QY 564 DPNAYIQELQKVLAPYARIFLRLPQVDTTGTGFKIQKTRLQREGFPDROTSDRLFLDL 623

Db 608 DGOKLQHVRSWLPAYATPHFIRIQDSLEITNTYKLVKSQALREGFDVGIADPLYLIDN 667

QY 624 KOGHYLPLNEAVYTRICSGAFAL 646

Db 668 KAETFRSLMPDVYQAVCEGTWKL 690

RESULT 15

O88694

ID O88694 PRELIMINARY; PRT: 662 AA.

AC O88694;

DT 01-NOV-1998 (Tremblrel. 08, Created)

DT 01-AUG-1999 (Tremblrel. 11, Last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)

DE FATTY ACID TRANSPORT PROTEIN 5 (VERY-LONG-CHAIN FATTY ACID TRANSPORT PROTEIN 5) (VERY-LONG-CHAIN ACYL-COA SYNTHETASE RELATED SLC27A5 OR VLACS).

DE ACID TRANSPORT PROTEIN 5 (VERY-LONG-CHAIN FATTY ACYL-COA SYNTHETASE RELATED SLC27A5 OR VLACS).

GN SLC27A5 OR VLACS.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=98337965; PubMed=9671728;

RX Hirsch D., Stahl A., Lodish H.F.;

RT "A family of fatty acid transporters conserved from mycobacterium to man.";

RL Proc. Natl. Acad. Sci. U.S.A. 95:8625-8629(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C; TISSUE=LIVER;

RX MEDLINE=98308102; PubMed=9642112;

RA Berger J., Truppe C., Neumann H., Forss-Petter S.;

RT "A novel relative of the very-long-chain acyl-CoA synthetase and fatty acid transporter protein genes with a distinct expression pattern.";

RL Biochem. Biophys. Res. Commun. 247:255-260(1998).

CC -!- FUNCTION: INVOLVED IN TRANSLLOCATION OF LONG-CHAIN FATTY ACIDS ACROSS THE PLASMA MEMBRANE. MAY PLAY A PIVOTAL ROLE IN REGULATING AVAILABLE LONG-CHAIN FATTY ACID SUBSTRATES FROM EXOGENOUS SOURCES IN TISSUES UNDERGOING HIGH LEVELS OF BETA-OXIDATION OR TRIGLYCERIDE SYNTHESIS.

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PLASMA MEMBRANE.

CC -!- TISSUE SPECIFICITY: LIVER, BUT NOT IN FETAL LIVER. LOW LEVELS IN BRAIN, LUNG, TESTES, SPLEEN, AND SKELETAL MUSCLE.

CC -!- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT COVALENT BINDING OF AMP TO THEIR SUBSTRATE.

DR EMBL: AF072760; AAC40189.1;

DR EMBL: AJ223959; CAAL1688.1; ALT_INT.

DR MGD; MGI:1347100; SLC27a5.

DR InterPro: IPR000873; AMP-bind.

DR Pfam: PF00501; AMP-binding; 1.

DR PROSITE: PS00455; AMP_BINDING; 1.

KW Glycoprotein; Lipid transport; Transmembrane; Signal; Transport.

FT SIGNAL 1 26 POTENTIAL.

FT CHAIN 27 662 FATTY ACID TRANSPORT PROTEIN 5.

FT TRANSMEM 28 48 POTENTIAL.

FT TRANSMEM 156 175 POTENTIAL.

FT TRANSMEM 312 332 POTENTIAL.

FT CARBOHYD 533 533 N-LINKED (GLCNAC...) (POTENTIAL).

FT CONFLICT 1 1 M -> MGWKLTLTLLLLVGLGQPPWPAAM (IN REF. 2).

FT CONFLICT 61 61 K -> I (IN REF. 2).

FT CONFLICT 381 381 T -> N (IN REF. 2).

FT CONFLICT 541 541 C -> S (IN REF. 2).

FT CONFLICT 661 661 N -> K (IN REF. 2).

SQ SEQUENCE 662 AA; 73251 MW; 1D7BAFE29F6D2712 CRC64;

Query Match 29.0%; Score 977.5; DB 11; Length 662;

Best Local Similarity 37.5%; Pred. No. 6e-66;

Matches 259; Conservative 104; Mismatches 243; Indels 85; Gaps 20;

QY 12 VSLALLW-----LLGLPW--TWS-----AAAALGVV-----GSGGWREL- 44

Db 1 MALALRWELGDPTCLVLLGLALLGRPWISSWMPHWSLVGAALTLLPPLPPPPGLRWLH 60

QY 45 RIVCKTARRDLGLSLVLRLELRRHORAGHTIPRFQAVQVQ-----PERALVDAGT 100

Db 61 KDVAFTEKMLFYGL---KFRRLNKH-----PETVDALERQALPDRVLAIVCTGS 110

QY 101 -GECWTFALDAYS-----NAVANLFRQLGFAPGDVVAIFL--EGRPEVGLW 145

Db 111 EGSSITNSQLDARSCQAAMVYLKAKLDVIONTR-----DAAALVLPLSKTISALSVF 163

QY 146 LGLAKAGMEALLNVNLRRLREPLAFCLGTSGAKALIFGGEWAAVAEVSCH-LGKSLIKPC 204

Db 164 LGLAKLCPVAVINPHSRGMPLLHSYRSSGASVLIIVDPDLENLEVLPLKLAENIHCFY 223

QY 205 SGDLGPEGILPDTHLLDPLKKEASTPL-----AQIPSKGMDRLFYIYTSCTGLPKAA 259

Db 224 LGHSSP---TPGVEALGASLDAAPSDVPASLRATIKWK---SPAIFITSGTGLPKPA 277

QY 260 IVVHSRYRMA---AFGHAYRMOAADVLYDCLPLYHSAGNIIGVQCCLLYGLTVVLRKK 316

Db 278 ILSHERVIOQVNVLSF---CCGRADDVYDVLPLYHTIGLVGLGLOVGCATCVLAPK 333

QY 317 FSASRWDCCIKYNTVQYIGECRYLLKOPVREARRHRVRLAVGNGLRPAIWEFTE 376

Db 334 FSASRFAECROHGVTVILYVGEILRYLCNVPEQEDKIHTVRLAMGTGLRANVKNFQ 393

QY 377 REGVRQIGEFYGATECNCISIANMDGKVGSCGFNSRILPHYPIRLVKVNETDWELLRDAQ 436

Db 394 REGPIRIWEFYGSTEGNVGLMNYVGHCGAVGRTSCILRLMTPFELVQDIETAEPLRDKQ 453

QY 437 GLCIPQAGEPGLLVGQINQODPLRRFDGVYVSESATSKIAHSVFSKDSAYLSGSDVLM 496

Db 454 GFCIPVEPKPGLLTLYKRNQNPGLYRG--SQAESNRKLVANVRVGGDYFFNGDVLTL 511

QY 497 DELGYMYFRDRSGDTRWRGNSVTEVEGVSRLGLQTDVAVYGVAVGVGKAGMAAV 556

Db 512 DQEGFFYQDRGLGDTFRWKNSTREVEGVSILDFLEEVNIGVYVPGCEGKVGMAAV 571

QY 557 -ADPHSLDPAIYQELQKVLAPYARIFLRLPQVDTTGTGFKIQKTRLQREGFPDROTSD 615

Db 572 KLAPGKTFDQOKLYQHVRSWLPAYATPHFIRIQDSLEITNTYKLVKSRLVRGFDVGIIA 631

QY 616 DRLFFDLKOGHYLPLNEAVYTRICSGAFAL 646

Db 632 DPLYLNDKQATFRSLMPDVYQAVCEGTWNL 662

Search completed: March 6, 2002, 13:42:04

Job time: 215 sec

QY	564	DENATVQLQVLKVPARPIFLRLLPOVDVTGTFIKTKRLQRQEGDPPROTSDRLFELDN	823
Db	608	DGEKIYHVRRAWLFPAYATPHFIQIDAMENVSTFKLMKTRLVEGENGVIGVDPDLFVDN	667
QY	624	KOGHYLPNEAVYTRICSGAFAL	646
Db	668	RAQSFRPLTAEMYQAVCEGTWRL	690
RESULT	14		
ID	Q9ES38	PRELIMINARY;	PRT; 690 AA.
AC	O9ES38;		
DT	01-WAR-2001 (TremBLrel. 16, Created)		
DT	01-WAR-2001 (TremBLrel. 16, Last sequence update)		
DT	01-JUN-2001 (TremBLrel. 17, Last annotation update)		
DE	BILE ACID COA LIGASE.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;		
NCBI_Taxid	10116;		
RP	[1]		
RC	SEQUENCE FROM N.A.		
RC	STRAIN=SPRAGUE-DAWLEY;		
RA	Palany C.N., Xie X., Wheeler J., Wang J., Barnes S.;		
RA	"Molecular Cloning and expression of rat liver bile acid CoA ligase.";		
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF242189; AAG09770.1; -		
DR	InterPro; IPR000873; AMP-blind.		
DR	ProSite; PS00455; AMP-BINDING; 1.		
KW	Ligase.		
SQ	SEQUENCE 690 AA; 76265 MW; D5BEB8317758DA59 CRC64;		
Query Match	29.5%;	Score 993.5;	DB 11; Length 690;
Best Local Similarity	37.9%;	Pred. No. 3.9e-67;	
Matches	259;	Conservative 101;	Mismatches 258; Indels 65; Gaps
QY	10	SVVSLALWLGLGP-----WTWSAAALGVVV---GSGGWRF	43
Db	27	AATALARWFLGDPTCFVLLGLAPLRPWTSIIHPWLSLAAALFTLSLLP RPPELRW	86
QY	44	LRIVCKTARRDLF--GLSVLRVRLELRHRORAGHTIPRIQAVVQRQ----PERIALYDA	98
Db	87	LHKDVAFAKLUFTGLN----LRRRLNRHP-----PELFVDALEQAQARPQDALVCT	136
QY	99	GTEGC-WTFAQLDAYS-NAVANLFRQLGFA-----PGDVVAIFLEGCP-EFYGLMWLGAK	150
Db	137	GSEGCISITNELNAKACAQAAWALKAKEATIQEDKGATAILVLPKSISALSIFYGLAK	196
QY	151	AGMEALLNVNLREPLAFCLTGTSKAKALIFGGEMVAAVAESVGH-LGKSLIKFCSGDLG	209
Db	197	LGPVAVINPHRGMPLLHSVQSSCASVLI VDPDLQENLEVLPKLLAEINRCIFYLGHS	256
QY	210	PEGILPDTHLLDPLKEASTAPLAIPSK-----GMDDRIFYIYTSCTGLPKAALVWHIS	264
Db	257	F---TPCGVALGAALDAAPSDB---VPAKLRLANKWKSPAIITYTSCTGLPKPALISHE	310
QY	265	RYRMAAFGHYAYMOAADVLDCLPLYHSAGNIIGVQCCLIYGLTVVLRKKKSASFWD	324
Db	311	RVLOMSNVLSFCGR-TADDVVYNVPLYHSMGLVGLGCIQLGATCVLAPKFSASRYWA	369
QY	325	DCIKYNTVVQYTGECIRYLLKQPVREARRHRVRLAVNGLRPAINEEETFERFGVRQIG	384
Db	370	ECROYSVTVVLYGVEVLYLCNVNPGPEDKKHTVFALONGLRADYWENFOQRFQIOIW	423
QY	385	EYFGATPCNCSTIANMGKVSGGFNSRIPLPHYPIYLRVKVNEDTMELLRDAQGLICPOA	444
Db	430	ELYGSTEGNGLMYNYGHCGAVGKTSCEFTRLMLTPLVELVOFDIETAEPYRDQKGFIPVET	483
QY	445	GEPLLVGQIQNOODPLRRFDYGYVSSESATSKKTAHSVSKDSAYLSGDLVVMDELGYMF	511

"A family of fatty acid transporters conserved from mycobacterium to man.";
Proc. Natl. Acad. Sci. U.S.A. 95:8625-8629(1998).
CC -1- FUNCTION: INVOLVED IN TRANSLLOCATION OF LONG-CHAIN FATTY ACIDS
ACROSS THE PLASMA MEMBRANE. MAY PLAY A PIVOTAL ROLE IN REGULATING
CC IN TISSUES UNDERGOING HIGH LEVELS OF BETA-OXIDATION OR
CC TRIGLYCERIDE SYNTHESIS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PLASMA MEMBRANE.
CC -1- TISSUE SPECIFICITY: LUNG, LIVER, AND TESTIS.
CC -1- SIMILARITY: TO OTHER ENZYMS WHICH ACT VIA AN ATP-DEPENDENT
CC COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
CC EMBL: AF072758; AAC40187.1; -.
DR MGD; MGI:1347358; SLC27a3.
DR InterPro: IPR000873; AMP-bind.
DR Pfam: PF00501; AMP-binding; 1.
DR PRINTS: PR00154; AMPBINDING
DR PROSITE; PS00455; AMP_BINDING; 1.
KW Glycoprotein; Lipid transport; Transmembrane; Transport.
FT NON_TER 1 1
FT TRANSMEM 99 119 POTENTIAL.
FT TRANSMEM 262 282 POTENTIAL.
FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 614 AA; 67041 MW; 33C2A558CDD9D989 CRC64;

Query Match 32.3%; Score 1090; DB 11; Length 614;
Best Local Similarity 40.9%; Pred. No. 1.4e-74;
Matches 247; Conservative 92; Mismatches 205; Indels 60; Gaps 11;
QY 85 VVQPERKALVDAGTGEWTFQALDAYSNVAVNLF-RQLGF----- 125
DB 21 LAREOPTHTFLING--AQRFSAEARESNRIARAFTRARGWTGRRGSGRGSTEGARV 78
QY 126 -----APGDVAIFLEGREFVGLWLGLAKAGMEALLNVLNRREPLA 168
DB 79 APPAGDAARGTTAPPLAGATVALLPAGDFLWIFGLAKAGLRTAFVPTALRRGPLL 138
QY 169 FCLGTSGAKALIFGEMVAAY-AEVSGLHGLSKLIFKFCGDLGPGILPDTHL--LDPLLK 225
DB 139 HCLRCGASALVATEFELESLEPDLPALRMLGLHWATG-----PETNVAGISNLLS 190
QY 226 EASTAPLAQIFS-----KGMDDRLFIYITSGTGLPKAAIVHVSRYRMAAFHHYRMQ 280
DB 191 EAADQVDFEVPVGYLSAPQNMIDTCLYIFTSGLTPKAAISHLVKVLQCGQF-YHLGCVH 249
QY 281 ADVLVDCPLVHSAGNIIGVQCCLYGLTVVLRKKFSASRFDWDCIKYNTVQYIGEI 340
DB 250 QEDVIYALPLVHMSGSLGIVGCLGICATVVLKPKFSASQFWDCCQKHRTVTVYIGEL 309
QY 341 CRYLLKQPVREARRHRYLAVGNGLRPAIWEETFERFVGRIQIGEFYGATCNCISANMD 400
DB 310 CRYLVNQPSKAEFDHKVRLAVGSLRPDWTWERFLRRFGPLQLILETYGTEGNVATFNYT 369
QY 401 KGKVGCGFNRLPHVYIRLVKVNEDTWELLRDAQGLICPCOAGEPLLVGQINCOODPL 460
DB 370 GRQAVGRASWLYKHIFPFLSRLYDVMTCPEIRNAQGHMTTSPGEPGLLVAPVSOQSP- 428
QY 461 RRFDCGVSSATSK-KIAHSVFSKGSAYLSGDLVMDDELGYMYFRDRSGDTFRWRGSEV 519
DB 429 --FLGAGAPELAKOKLLKDVFSWGDVFNFTGDLVLCDEQGLFHDHDTGRTIRWKGENV 486
QY 520 STTEVEGVSRLSLGGTDAVYGVAVPGVEGKAGMAVA-DPHSLLDPNNAIYQELQKVLAP 578
DB 487 ATTEVAEVLDTDFLQEVNIYGVTPGHEGRAGMAALRRPQALNLVQLYSHVSENLP 546
QY 579 YARPIFLRLPQVDTTGTFTKIQKTRLOREGFDPQTSDELFLDLKQGHVPLNEAVYTR 638
DB 547 YARPRELRQESLATTETFKQKVRMANEGFDFSVLSDPVLYDQDQIGAYLPLTPARYSA 606
QY 639 ICSSG 642
DB 607 LLSG 610

RESULT 10
Q9Y2P4 PRELIMINARY; PRT; 619 AA.
ID Q9Y2P4;
AC Q9Y2P4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE VERY LONG-CHAIN ACYL-COA SYNTHETASE HOMOLOG 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP Steinberg S.J., Watkins P.A.;
RT "Human Very Long-Chain Acyl-CoA Synthetase Homolog 1.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF064254; AAD29443.1; -.
DR InterPro: IPR000873; AMP-bind.
DR Pfam: PF00501; AMP-binding; 1.
DR PROSITE; PS00455; AMP_BINDING; 1.
SQ SEQUENCE 619 AA; 70111 MW; 20264CE3FBB44FF5 CRC64;
Query Match 32.1%; Score 1083; DB 4; Length 619;
Best Local Similarity 37.0%; Pred. No. 4.9e-74;
Matches 243; Conservative 125; Mismatches 228; Indels 60; Gaps 14;
QY 5 GAGAAVSVALILWLILGLPWTWSAAAALGVVYSGGWRFLRVICVKTARTDRDLFGLSVLIRV 64
DB 10 GAG---MVLHFLQLKLPFFW-----DDFWFLKV-----VLIII 42
QY 65 RLRLRHQAGH--TIPRFQAVQVQPERLALVDAGTGEWTFQALDAYSNVAVNLF-R 121
DB 43 R--LKYEKRGELVTLVDKFLSHAKRQPKPFII--YEGDIITYQDVKRKRSHVAVFLN 98
QY 122 QLGFAFGDVVAIFLEGREFVGLWLGLAKAGMEALLNVLNRREPLAFCLGTSGAKALIF 181
DB 99 HSELKKGDTVALMSNEPDEFVHWFGGLKGLCVAFPLNTNIRSNLLNLCIRACGPRALV 158
QY 182 GGEVAAVAEVSGLHGLSKLIFKFCGDLGPGILPDTHLLDPLLKEASTAPLAQIIPSG-- 239
DB 159 GADLGTVEILPSLSENISVWGMKDSVPQGV-----SLKEKLSLTPDPEVPRSHV 211
QY 240 ---MDRLFIYITSGTGLPKAAIVHVSRYR---MAAFHHYRMAADVLVDCPLY 292
DB 212 VSLKSTCLYIFTSGLTPKAAVISQLQVLRGSVILWAFGCTAH-----DIVYITLPLY 266
QY 293 HSAGNIIGVQCCLYGLTVVLRKKFSASRFDWDCIKYNTVQYIGEIYCRYLLKQPVREA 352
DB 267 HSSAAILIGSCVELGATCVLKKKFSASQFWSCKKYDVTVFQYIGELCRYLCKQSKREG 326
QY 353 ERHVRVLAVGNGLRPAIWEETFERFVGRIQIGEFYGATCNCISANMDKVGSCGNSRI 412
DB 327 EKQHKVRLAINGIRSDVWREFLDKFNKVCLEYAATESISFMNYTGRIGAIGRTNLF 386
QY 413 LPHVYIRLVKVNEDTWELLRDAQGLICPCOAGEPLLVGQINCOODPLRREDGVSE-SA 471
DB 387 YKLLSTFDLIKYDFQKDEPNRNEQGWCIHVKKGEPGLLISRVNAKNP---FFYAGPYKH 443
QY 472 TSKKIAHSVFSKGSAYLSGDLVMDDELGYMYFRDRSGDTFRWRGENVSTTEVEGVSRL 531
DB 444 TKDCLLDVFKGDDVYINTGDLIVQDQDNFLYFWDRTGDTFRWKGENVATTEVADVIGML 503
QY 532 LGQTDVAVYGVAVPGVEGKAGMAA-VADPHSLLDPNNAIYQELQKVLAPYARPIFLRLPQ 590
DB 504 DFIQEVAVYGVAVISYEGRAGMASIILKPNKTSIDLEKVEYVQVVTFLPAYACPRFLRQEK 563
QY 591 VDTTGTFTKIQKTRLOREGFDPQTSDELFLDLKQGHVPLNEAVYTRICSGAFAL 646
DB 564 MEATGTTKLLKHQLVEDGFNPLKISEPLIYMDNLKSYVLLTRELVDQIMLEIKL 619

	Query Match	37.0%;	Score 1246;	DB 11;	Length 334;
	Best Local Similarity	69.6%;	Pred. No. 7e-87;	Mismatches	0;
	Matches 229;	Conservative 41;			
Qy	314	RKFSASRFWDDCIKYNCTVVOYGEICRYLLKQPVEARERHRYVLAVNGCLRPAIWE	373		
Db	2	RKFSASRFWDDCIKYNCTVVOYGEICRYLLNQPPEAESRHKVRMALNGLSROSITWD	61		
Qy	374	FTREFGYROIIEGYGATECNCSIANMDGKVGSGCFNSRLPHVYPIRLVKVNEDTME	433		
Db	62	FSSRFHPQVAEFGATECNCSLGNFDSRVGACGFNSRLSFVYPIRLVRVNEDTME	121		
Qy	434	DAOGLCIPCQAGBGLLVGOINQODPLRPFDGTVSSEATSKKIAHSVFSKGSAYLSGDV	493		
Db	122	GPDCGVCIPCQGPQGPQVLGRIIQODPLRPFDGTVLNGANNKKIANDVFVKKGQAYLTGDV	181		
Qy	494	LVMDELGYMYFDRDRSGDTFRWRGENYSTTEVEGVLSSLRLGQTDVAIVGYVAPVPGVEGKAM	553		

[illegible]

QY 125 FAPGDVAIFLEGRPEFVGLWGLAKAGMEALLNVLNRREPLAFCLGTSGAKALIFGGE 184
 Db 123 LAGSDVAALFMENRFEVGLWGLMAKLGVEAALINTLNRDALLCLTTSARALVFGSE 182
 QY 185 MVAANAESVGHLCGLKSLKFCSDGLGPEGLPDTHLLDPLLEKASTAPLAQIPSKGMDRL 244
 Db 183 MASAICEVHASDPDSLFCSGSWEPGAVPPSTEHLDPDLKDA-PKHLPSPCDPKGFTDKL 241
 QY 245 FYIYSGTGLPKAAIVVHRSYRMAAFGHAYRMAADVLYDCLPLYHSAAGNIIGVQC 304
 Db 242 FYIYSGTGLPKAAIVVHRSYRMAALVYGFGRMPNDIVYDCLPLYHSAAGNIIGVQC 301
 QY 305 LIYGLTVVLRKFSASREDDCIKYNCTVQYIGICRYLLKQPVREARRHVRVLAAGN 364
 Db 302 LHGNTVVRKFSASREDDCIKYNCTVQYIGICRYLLKQPVREARRHVRVLAAGN 361
 QY 365 G-----LRPAI-----WEEFTFRFVRQIGEFYGEATECNCSTANMDGVKSGCFNSRI 412
 Db 362 ASGSPSGTFFAASYPRWLSST-----GPECNCSLGNFDSQVAGCFNSRI 408
 QY 413 LPHYVPIRLVKNEDTMELLRDAOGLCIPQAGEPGLLVGOINQDDPLRRFDGVVSESAT 472
 Db 409 LSFVPIRLVKNEDTMELIRGPDGVCIPQAGEPGLLVGOINQDDPLRRFDGVVSESAT 468
 QY 473 SKKIAHSFSGDSAYLSGDLVMDGLYMYFRDRSGDTRFRWGENVSTTEVEGVLSRL 532
 Db 469 NKKIADVFKGDAQYLTGDLVMDGLYMYFRDRSGDTRFRWGENVSTTEVEGVLSRL 528
 QY 533 QOTDVAIVGAVPGEKAGMAAVADPHSLDPAIYQELQKVLAPYARPIFLRLPOVD 592
 Db 529 DMADVAVGVPEVTEGREGMAAVASPTGNCDLERFAQVLEKELPLYARPIFLRLPELH 588
 QY 593 TTGFETKQKLOREGDPDPRQTSRDLFLDKOGLYPLNEAVYTRICSG 642
 Db 589 KTGYKFKQKLEKAEADPAIVKTRC-SIYIERGVYPLDQEAYSRIQAG 637

RESULT 2

ID 088562 PRELIMINARY; PRT; 506 AA.
 AC 088562;
 DT 01-NOV-1998 (TEMBLrel. 08, Created)
 DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
 DE FATTY ACID TRANSPORT PROTEIN 4 (FATP4) (LONG-CHAIN FATTY ACID TRANSPORT PROTEIN 4) (FRAGMENT).
 GN SLC27A4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98337965; PubMed=9671728;
 RA Hirsch D., Stahl A., Lodish H.F.;
 RT "A family of fatty acid transporters conserved from mycobacterium to man.";
 RT Proc. Natl. Acad. Sci. U.S.A. 95:8625-8629(1998).
 RL -!- FUNCTION: INVOLVED IN TRANSLLOCATION OF LONG-CHAIN FATTY ACIDS ACROSS THE PLASMA MEMBRANE. MAY PLAY A PIVOTAL ROLE IN REGULATING AVAILABLE LONG-CHAIN FATTY ACID SUBSTRATES FROM EXOGENOUS SOURCES IN TISSUES UNDERGOING HIGH LEVELS OF BETA-OXIDATION OR TRIGLYCERIDE SYNTHESIS.
 CC -!- TISSUE SPECIFICITY: HEART, BRAIN, LUNG, LIVER, AND KIDNEY.
 CC -!- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
 CC EMBL; AF072759; AAC40188.1; -.
 DR MGD; MGI:1347347; SLC27A4.
 DR InterPro; IPR000873; AMP-bind.
 DR Pfam; PF00501; AMP-binding; 1.
 DR PRINTS; PR00154; AMPBINDING.
 DR PROSITE; PS00455; AMP_BINDING; 1.
 KW Glycoprotein; Lipid transport; Transport.

FT NON_TER 1 1
 FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 378 378 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 506 AA; 56902 MW; 4EBBC80C2173326D CRC64;

Query Match 51.0%; Score 1719.5; DB 11; Length 506;
 Best Local Similarity 65.3%; Pred. No. 1.1e-122;
 Matches 324; Conservative 65; Mismatches 106; Indels 1; Gaps 1;

QY 147 GLAKAGMEALLNVLNRREPLAFCLGTSGAKALIFGEMVAVAESVGHLSKSLKFCSG 206
 Db 8 GMAKLGVEAALINTLNRDALLCLTTSARALIFGEMASAICEHASELTLSLFCSG 67
 QY 207 DLGPEGILPDTHLLDPLLEKASTAPLAQIPSKGMDRLFYIYTSGTGGLPKAAIVVHRSY 266
 Db 68 SWEPSTVPVSTEHLDPLLEDA-PKHLPSHPDKGFTDKLEYIYTSGTGGLPKAAIVVHRSY 126
 QY 267 YRMAAFGHAYRMAADVLYDCLPLYHSAAGNIIGVQCILYGLTVVLRKFSASREWDCC 326
 Db 127 YRMAALVYGFGRMPNDIVYDCLPLYHSAAGNIIGVQCILYGLTVVLRKFSASREWDCC 186
 QY 327 IKYNCTVQYIGICRYLLKQPVREARRHVRVLAAGNGLRPAIWEETETEBGVQIGEF 386
 Db 187 IKYNCTVQYIGICRYLLKQPVREARRHVRVLAAGNGLRPAIWEETETEBGVQIGEF 246
 QY 387 YGATECNCISANNQKVGSCGPNRILPHVPIRLVKNEDTMELLRDAQGLCIPQAGE 446
 Db 247 YGATECNCISLGNFDSQVAGCFNSRIISFYVPIRLVKNEDTMELIRGPDGVCIPQAG 306
 QY 447 PGLLVGOINQDDPLRRFDGVVSESATSKKIAHSFSGDSAYLSGDLVMDGLYMYFRD 506
 Db 307 PGLLVGOINQDDPLRRFDGVVSESATSKKIAHSFSGDSAYLSGDLVMDGLYMYFRD 366
 QY 507 RSGDTRFRWGENVSTTEVEGVLSRLLGOTDVAIVGAVPGEKAGMAAVADPHSLDPA 566
 Db 367 RSGDTRFRWGENVSTTEVEGVLSRLLGOTDVAIVGAVPGEKAGMAAVADPHSLDPA 426
 QY 567 AIYQELQKVLAPYARPIFLRLPOVDTTGTFKIOKTRLOREGDPDPRQTSRDLFLDKO 626
 Db 427 SFAQTLKKELPLYARPIFLRLPELHKTGTFKQKLEKAEADPAIVKTRC-SIYIERGV 486
 QY 627 HYLPLNEAVYTRICSG 642
 Db 487 CYVALDQEAAYTRIQAG 502

RESULT 3

Q9W1V9
 ID Q9W1V9 PRELIMINARY; PRT; 671 AA.
 AC Q9W1V9;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
 DE CG3037 PROTEIN.
 GN CG3037.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 6, 2002, 13:38:29 ; Search time 28.8 Seconds
(without alignments)
3280.970 Million cell updates/sec

Title: US-09-405-504A-25
Perfect score: 3372
Sequence: 1 MRAPGAGAAVSVSLALLMLL.....HYLPNEAVYTRICSGAPAL 646

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL17: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phase: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1958	58.1	641	4	Q95186	Q95186 homo sapien
2	1719.5	51.0	506	11	O88562	O88562 mus musculu
3	1476.5	43.8	671	5	Q9WLV9	Q9WLV9 drosophila
4	1348.5	40.0	690	5	Q9VKU1	Q9VKU1 drosophila
5	1267.5	37.6	650	5	Q19878	Q19878 caenorhabdi
6	1257.5	37.3	655	5	O18916	O18916 caenorhabdi
7	1246	37.0	334	11	Q9CV67	Q9CV67 mus musculu
8	1245.5	36.9	661	5	Q9W185	Q9W185 drosophila
9	1090	32.3	614	11	O88561	O88561 mus musculu
10	1083	32.1	619	4	Q9Y2P4	Q9Y2P4 homo sapien
11	1082	32.1	730	4	Q9ERY5	Q9ERY5 homo sapien
12	1017.5	30.2	635	2	Q9A528	Q9A528 caulobacter
13	1007.5	29.9	690	11	Q9Y2P5	Q9Y2P5 homo sapien
14	993.5	29.5	690	11	Q9ES38	Q9ES38 rattus norv
15	977.5	29.0	662	11	O88694	O88694 mus musculu
16	915	27.1	258	4	Q9ETA1	Q9ETA1 homo sapien
17	899.5	26.7	597	2	O05307	O05307 mycobacteri
18	891	26.4	623	11	O88560	O88560 mus musculu
19	872	25.9	608	2	Q9HZV4	Q9HZV4 pseudomonas

20	829.5	24.6	402	4	Q9BTJ5	Q9BTJ5 homo sapien
21	747.5	22.2	643	3	O42633	O42633 cochllobolu
22	716.5	21.2	669	3	O60021	O60021 saccharomyc
23	410	12.2	555	2	O85737	O85737 streptomyce
24	377.5	11.2	504	2	O9Z1P5	O9Z1P5 rhizobium l
25	377	11.2	502	2	O33551	O33551 mycobacteri
26	372	11.0	532	2	P72007	P72007 mycobacteri
27	361	10.7	2723	2	O30479	O30479 streptomyce
28	351	10.4	523	2	O9AJS8	O9AJS8 thauera aro
29	346.5	10.3	503	2	O53306	O53306 mycobacteri
30	325	9.6	444	2	O9X4W6	O9X4W6 pseudomonas
31	323.5	9.6	549	2	O31826	O31826 bacillus su
32	321	9.5	535	2	O9KHL1	O9KHL1 streptomyce
33	320	9.5	593	1	O29233	O29233 archaeoglob
34	319	9.5	549	2	O9R9I5	O9R9I5 bacillus su
35	316	9.4	513	2	O07610	O07610 bacillus su
36	315	9.3	999	2	O33185	O33185 mycobacteri
37	309	9.2	496	2	O9A5P7	O9A5P7 caulobacter
38	307	9.1	486	2	O34837	O34837 bacillus su
39	305	9.0	560	2	P95227	P95227 mycobacteri
40	303.5	9.0	523	2	O32301	O32301 bacillus su
41	300.5	8.9	599	1	O9Y9K4	O9Y9K4 aeropyrum p
42	300.5	8.9	3583	2	O45675	O45675 bacillus su
43	300	8.9	504	2	O9F7P5	O9F7P5 uncultured
44	295.5	8.8	530	2	O9A9L4	O9A9L4 caulobacter
45	294	8.7	514	10	Q9SMT7	Q9SMT7 arabidopsis

ALIGNMENTS

RESULT	1
Q95186	PRELIMINARY; PRT; 641 AA.
ID	O95186
AC	O95186; (TREMREL. 10, Created)
DT	01-MAY-1999 (TREMREL. 10, Last sequence update)
DT	01-MAY-1999 (TREMREL. 10, Last sequence update)
DT	01-JUN-2001 (TREMREL. 17, Last annotation update)
DE	FATTY ACID TRANSPORT PROTEIN.
GN	FATP.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=HEART;
RX	MEDLINE=99056471; PubMed=9878842;
RA	Fitscher B.A., Riedel H.D., Young K.C., Strommel W.
RT	"Tissue distribution and cDNA cloning of a human fatty acid transport protein (hsFATP4)."
RL	Biochim. Biophys. Acta 1443:381-385(1998).
DR	EMBL: AF055899; AAD11623.1;
DR	InterPro: IPR000566; Lipocln_cytFABP.
DR	InterPro: IPR000873; AMP-bind.
DR	Pfam: PF00501; AMP-binding; 1.
DR	PROSITE: PS00455; AMP_BINDING; 1.
DR	PROSITE: PS00213; LIPOCALIN; UNKNOWN_1.
SQ	SEQUENCE 641 AA; 71431 MW; 8C24F76C9BF81378 CRC64;

Query Match 58.1%; Score 1958; DB 4; Length 641;
Best Local Similarity 58.6%; Pred. No. 1.1e-140;
Matches 381; Conservative 88; Mismatches 153; Indels 28; Gaps 6;

Qy	5	GAGAAVSVSLALLMLLGLPTWTSAAALGVVGGWRRFLRVICVTKARRDLFGLSVLIRY 64
Db	4	GASLVGLVLFKSL-VKLIPWTQVGSLLFLYLGGWRRFLRVFKTIRRDIFGGLVLLKV 62
Qy	65	RLELRHQRAGHTIPRIFQAVVQPERLALVDAGTGCWTFQALDAYSANANFLRQLG 124
Db	63	KAKVQCQCQRRTVPILFASTVRRHPDKTALIFEFTDTHWTFRLQDEYSSVANFLOARG 122